L6pu 1644

1600

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RAW SEQUENCE LISTING                        DATE: 04/23/2003
PATENT APPLICATION:  US/09/905,589A         TIME: 13:02:46

Input Set : N:\EBONY'S\EP.txt
Output Set: N:\CRF4\04232003\I905589A.raw
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 3 <110> APPLICANT: Chadwick, Brian Paul
 4        Frischauf, Anna Maria
 6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE POLYPEPTIDES
AND NUCLEIC
 7        ACIDS
 9 <130> FILE REFERENCE: 28110/36120D
11 <140> CURRENT APPLICATION NUMBER: 09/905,589A
12 <141> CURRENT FILING DATE: 2001-07-13
14 <150> PRIOR APPLICATION NUMBER: 09/240,639
15 <151> PRIOR FILING DATE: 1999-01-29
17 <160> NUMBER OF SEQ ID NOS: 32
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 2762
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo Sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (232)..(1599)
29 <223> OTHER INFORMATION:
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35 aagaccggct gccgcctgct ccccggaaaa gggcactcgt ctccgtgggt gtggcggagc   120
37 gcgcggtgca tggaatgggc tatgtgaatg aaaaaaggta tccgttatga aacttccaga   180
39 aaaacgagct acatttttca gcagccgcag cacggtcctt ggcaaacaag g atg aga     237
40                                                         Met Arg
41                                                           1
43 aaa ata tcc aac cac ggg agc ctg cgg gtg gcg aag gtg gca tac ccc     285
44 Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
45         5                   10                  15
47 ctg ggg ctg tgt gtg ggc gtg ttc atc tat gtt gcc tac atc aag tgg     333
48 Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
49         20                  25                  30
51 cac cgg gcc acc gcc acc cag gcc ttc ttc agc atc acc agg gca gcc     381
52 His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
53 35                  40                  45                  50
55 ccg ggg gcc cgg tgg ggt cag cag gcc cac agc ccc ctg ggg aca gct     429
56 Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
57                     55                  60                  65
59 gca gac ggg cac gag gtc ttc tac ggg atc atg ttt gat gca gga agc     477
60 Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
61                 70                  75                  80
63 act ggc acc cga gta cac gtc ttc cag ttc acc cgg ccc ccc aga gaa     525
64 Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu
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65          85                  90                  95
67 act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt     573
68 Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu
69      100                 105                 110
71 tct gcc tat gct gat gat gtt gaa aag agc gct cag gga atc cgg gaa     621
72 Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu
73 115                 120                 125                 130
75 cta ctg gat gtt gct aaa cag gac att ccg ttc gac ttc tgg aag gcc     669
76 Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala
77              135                 140                 145
79 acc cct ctg gtc ctc aag gcc aca gct ggc tta cgc ctg tta cct gga     717
80 Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly
81          150                 155                 160
83 gaa aag gcc cag aag tta ctg cag aag gtg aaa gaa gta ttt aaa gca     765
84 Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala
85          165                 170                 175
87 tcg cct ttc ctt gta ggg gat gac tgt gtt tcc atc atg aac gga aca     813
88 Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr
89      180                 185                 190
91 gat gaa ggc gtt tcg gcg tgg atc acc atc aac ttc ctg aca ggc agc     861
92 Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser
93 195                 200                 205                 210
95 ttg aaa act cca gga ggg agc agc gtg ggc atg ctg gac ttg ggc gga     909
96 Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly
97              215                 220                 225
99 gga tcc act cag atc gcc ttc ctg cca cgc gtg gag ggc acc ctg cag     957
100 Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln
101              230                 235                 240
103 gcc tcc cca ccc ggc tac ctg acg gca ctg cgg atg ttt aac agg acc    1005
104 Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr
105          245                 250                 255
107 tac aag ctc tat tcc tac agc tac ctc ggg ctc ggg ctg atg tcg gca    1053
108 Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala
109      260                 265                 270
111 cgc ctg gcg atc ctg ggc ggc gtg gag ggg cag cct gct aag gat gga    1101
112 Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly
113 275                 280                 285                 290
115 aag gag ttg gtc agc cct tgc ttg tct ccc agt ttc aaa gga gag tgg    1149
116 Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp
117              295                 300                 305
119 gaa cac gca gaa gtc acg tac agg gtt tca ggg cag aaa gca gcg gca    1197
120 Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala
121              310                 315                 320
123 agc ctg cac gag ctg tgt gct gcc aga gtg tca gag gtc ctt caa aac    1245
124 Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn
125          325                 330                 335
127 aga gtg cac agg acg gag gaa gtg aag cat gtg gac ttc tat gct ttc    1293
128 Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe
129      340                 345                 350
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131 tcc tac tat tac gac ctt gca gct ggt gtg ggc ctc ata gat gcg gag      1341
132 Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu
133 355             360             365             370
135 aag gga ggc agc ctg gtg gtg ggg gac ttc gag atc gca gcc aag tac      1389
136 Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr
137             375             380             385
139 gtg tgt cgg acc ctg gag aca cag ccg cag agc agc ccc ttc tca tgc      1437
140 Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys
141             390             395             400
143 atg gac ctc acc tac gtc agc ctg cta ctc cag gag ttc ggc ttt ccc      1485
144 Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro
145         405             410             415
147 agg agc aaa gtg ctg aag ctc act cgg aaa att gac aat gtt gag acc      1533
148 Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
149     420             425             430
151 agc tgg gct ctg ggg gcc att ttt cat tac atc gac tcc ctg aac aga      1581
152 Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
153 435             440             445             450
155 cag aag agt cca gcc tca tagtggccga gccatccctg tccccgtcag           1629
156 Gln Lys Ser Pro Ala Ser
157             455
159 cagtgtctgt gtgtctgcat aaaccctcct gtcctggacg tgacttcatc ctgaggagcc   1689
161 acagcacagg ccgtgctggc actttctgca cactggctct gggacttgca gaaggcctgg   1749
163 tgctgccctg gcatcagcct cttccagtca catctggcca gagggctgtc tggacctggg   1809
165 ccctgctcaa tgccacctgt ctgcctgggc tccaagtggg caggaccagg acagaaccac   1869
167 aggcacacac tgaggggggca gtgtggctcc ctgcctgtcc catccccatg ccccgtccgc   1929
169 ggggctgtgg ctgctgctgt gcatgtccct gcgatgggag tcttgtctcc cagcctgtca   1989
171 gtttcctccc cagggcagag ctcccccttcc tgcaagagtc tgggaggcgg tgcaggctgt   2049
173 cctggctgct ctggggaagc cgagggacag ccataacacc cccgggacag taggtctggg   2109
175 cggcaccact gggaactctg gacttgagtg tgtttgctct tccttgggta tgaatgtgtg   2169
177 agttcaccca gaggcctgct ctcctcacac attgtgtggt ttggggttaa tgatggaggg   2229
179 agacacctct tcatagacgg caggtgccca cctttcaggg agtctcccag catgggcgga   2289
181 tgccgggcat gagctgctgt aaactatttg tggctgtgct gcttgagtga cgtctctgtc   2349
183 gtgtgggtgc caagtgcttg tgtagaaact gtgttctgag ccccctttttc tggacaccaa   2409
185 ctgtgtcctg tgaatgtatc gctactgtga gctgttcccg cctagccagg gccatgtctt   2469
187 aggtgcagct gtgccacggg tcagctgagc cacagtccca gaaccaagct ctcggtgtct   2529
189 cgggccacca tccgcccacc tcgggctgac cccacctcct ccatggacag tgtgagcccc   2589
191 gggccgtgca tcctgctcag tgtggcgtca gtgtcggggc tgagcccctt gagctgcttc   2649
193 agtgaatgta cagtgcccgg cacgagctga acctcatgtg ttccactccc aataaaaggt   2709
195 tgacaggggc ttctccttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa           2762
198 <210> SEQ ID NO: 2
199 <211> LENGTH: 456
200 <212> TYPE: PRT
201 <213> ORGANISM: Homo Sapiens
203 <400> SEQUENCE: 2
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206 1               5               10              15
209 Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile
210         20              25              30
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RAW SEQUENCE LISTING   DATE: 04/23/2003
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Output Set: **N:\CRF4\04232003\I905589A.raw**

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213 Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg
214         35              40              45
217 Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly
218     50              55              60
221 Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala
222 65              70              75              80
225 Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro
226             85              90              95
229 Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro
230         100             105             110
233 Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile
234         115             120             125
237 Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp
238     130             135             140
241 Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu
242 145             150             155             160
245 Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe
246             165             170             175
249 Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn
250             180             185             190
253 Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr
254         195             200             205
257 Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu
258     210             215             220
261 Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr
262 225     \           230             235             240
265 Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn
266             245             250             255
269 Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met
270             260             265             270
273 Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys
274         275             280             285
277 Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly
278     290             295             300
281 Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala
282 305             310             315             320
285 Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu
286             325             330             335
289 Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr
290             340             345             350
293 Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp
294         355             360             365
297 Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala
298     370             375             380
301 Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe
302 385             390             395             400
305 Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly
306             405             410             415
309 Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val
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```
310              420               425               430
313 Glu Thr Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu
314          435               440               445
317 Asn Arg Gln Lys Ser Pro Ala Ser
318     450               455
321 <210> SEQ ID NO: 3
322 <211> LENGTH: 2797
323 <212> TYPE: DNA
324 <213> ORGANISM: Homo Sapiens
326 <220> FEATURE:
327 <221> NAME/KEY: CDS
328 <222> LOCATION: (83)..(1669)
329 <223> OTHER INFORMATION:
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W--> 332 <400> 3

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335 ctccgcacag ctaggagaaa ag atg ttc act gtg ctg acc cgc caa cca tgt     112
336                         Met Phe Thr Val Leu Thr Arg Gln Pro Cys
337                          1           5                   10
339 gag caa gca ggc ctc aag gcc ctc tac cga act cca acc atc att gcc     160
340 Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala
341          15                  20                  25
343 ttg gtg gtc ttg ctt gtg agt att gtg gta ctt gtg agt atc act gtc     208
344 Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val
345          30                  35                  40
347 atc cag atc cac aag caa gag gtc ctc cct cca gga ctg aag tat ggt     256
348 Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly
349          45                  50                  55
351 att gtg ctg gat gcc ggg tct tca aga acc aca gtc tac gtg tat caa     304
352 Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln
353      60                  65                  70
355 tgg cca gca gaa aaa gag aat aat acc gga gtg gtc agt caa acc ttc     352
356 Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe
357 75                  80                  85                  90
359 aaa tgt agt gtg aaa ggc tct gga atc tcc agc tat gga aat aac ccc     400
360 Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro
361                  95                  100                 105
363 caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg     448
364 Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly
365              110                 115                 120
367 cag gtt cca tcc cac ctc cac gga tcc acc ccc att cac ctg gga gcc     496
368 Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala
369          125                 130                 135
371 acg gct ggg atg cgc ttg ctg agg ttg caa aat gaa aca gca gct aat     544
372 Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn
373      140                 145                 150
375 gaa gtc ctt gaa agc atc caa agc tac ttc aag tcc cag ccc ttt gac     592
376 Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp
377 155                 160                 165                 170
379 ttt agg ggt gct caa atc att tct ggg caa gaa gaa ggg gta tat gga     640
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/23/2003
PATENT APPLICATION: **US/09/905,589A**   TIME: 13:02:47

Input Set : **N:\EBONY'S\EP.txt**
Output Set: **N:\CRF4\04232003\I905589A.raw**

<u>Invalid Line Length:</u>
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 6

VERIFICATION SUMMARY   DATE: 04/23/2003
PATENT APPLICATION: **US/09/905,589A**   TIME: 13:02:47

Input Set : **N:\EBONY'S\EP.txt**
Output Set: **N:\CRF4\04232003\I905589A.raw**

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L:332 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:329
L:664 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:661
L:924 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:921
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